

FIGURE 1

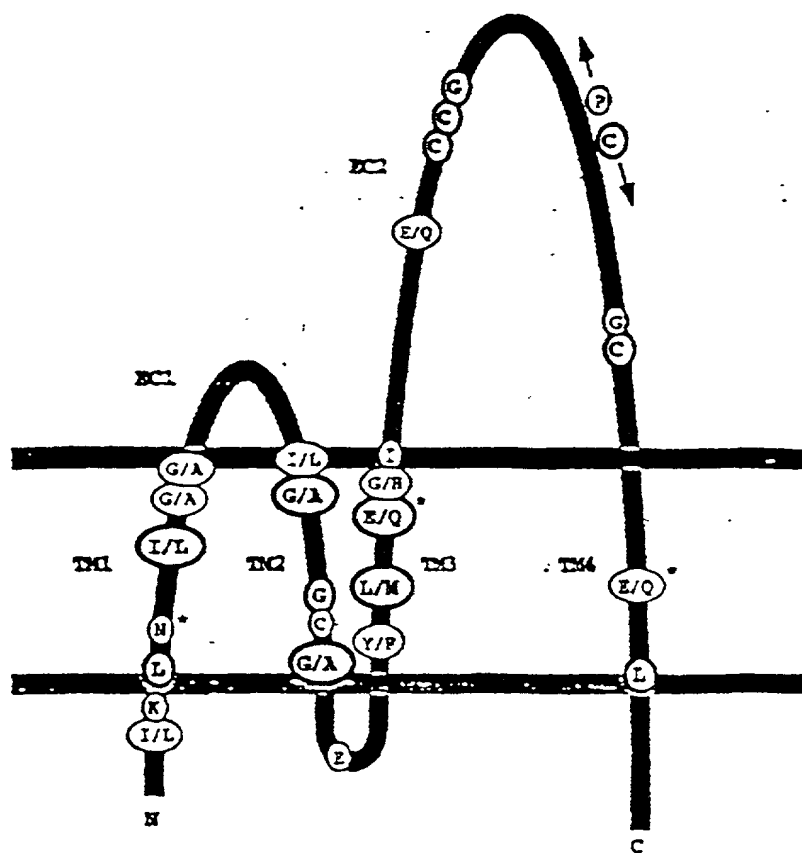


FIGURE 2A

1 CTTCTCGGC CGAGCCGGGC CGCGCGGCCG CTGCCGCCGC CGCGCGCGGA
GAAGGAGCCG GCTCGGCCCG GCGCGCCGGC GACGGCGGCG GCGCGCGCCT

+1]-----
51 TTCTGCTTCT CAGAAGATGC ACTATTATAG ATACTCTAAC GCCAAGGTCA
AAGACGAAGA GTCTTCTACG TGATAATATC TATGAGATTG CGGTTCCAGT

+1 -----
101 GCTGCTGGTA CAAGTACCTC CTTTTCAGCT ACAACATCAT CTTCTGGTTG
CGACGACCAT GTTCATGGAG GAAAAGTCGA TGTGTAGTA GAAGACCAAC
-3 <-----

+3]-----
+1 -----
151 GCTGGAGTTG TCTTCCTTGG AGTCGGGCTG TGGGCATGGA GCGAAAAGGG
CGACCTCAAC AGAAGGAACC TCAGCCCGAC ACCCGTACCT CGCTTTTCCC
-3 -----

+3 -----
+1 -----
201 TGTGCTGTCC GACCTCACCA AAGTGACCCG GATGCATGGA ATCGACCCTG
ACACGACAGG CTGGAGTGGT TTTACTGGGC CTACGTACCT TAGCTGGGAC
-3 -----

+3 -----
+1 -----
251 TGGTGCTGGT CCTGATGGTG GCGGTGGTGA TGTTCAACCT GGGGTTGCGC
ACCACGACCA GGACTACCAC CCGCACCACT ACAAGTGGGA CCCCAGCGG
-3 -----

+3 -----
+1 -----
301 GGCTGCGTGG GGGCTCTGCG GGAGAATATC TGCTTGCTCA ACTTTTCTG
CCGACGCACC CCCGAGACGC CCTCTTATAG ACGAACGAGT TGAAAAAGAC
-3 -----

+3 -----
+1 -----
351 TGGCACCATC GTGCTCATCT TCTTCCTGGA GCTGGCTGTG GCCGTGCTGG
ACCGTGCTAG CACGAGTAGA AGAAGGACCT CGACCGACAC CGGCACGACC
-3 -----

+3 -----
+1 -----
401 CCTTCCTGTT CCAGGACTGG GTGAGGGACC GGTCCCGGA GTTCTTCGAG
GGAAGGACAA GGTCTGACC CACTCCCTGG CCAAGGCCCT CAAGAAGCTC
-3 -----

+3 -----
+1 -----
451 AGCAACATCA AGTCCTACCG GGACGATATC GATCTGCAA ACCTCATCGA
TCGTTGTAGT TCAGGATGGC CCTGCTATAG CTAGACGTTT TGGAGTAGCT
-3 ----- {

+3 ----->
+1 -----
501 CTCCCTTCAG AAAGCTAACC AGTGCTGTGG CGCATATGGC CCTGAAGACT
GAGGGAAGTC TTTCGATTGG TCACGACACC GCGTATACCG GGAATTCTGA

FIGURE 2B

```
+1 -----  
551 GGGACCTCAA CGTCTACTTC AATTGCAGCG GTGCCAGCTA CAGCCGAGAG  
    CCCTGGAGTT GCAGATGAAG TTAACGTCGC CACGGTCGAT GTCGGCTCTC  
-----  
+1 -----  
601 AAGTGCGGGG TCCCCTTCTC CTGCTGCGTG CCAGATCCTG CGCAAAAAGT  
    TTCACGCCCC AGGGGAAGAG GACGACGCAC GGTCTAGGAC GCGTTTTTCA  
-----  
+1 -----  
651 TGTGAACACA CAGTGTGGAT ATGATGTCAG GATTGAGCTG AAGAGCAAGT  
    ACACTTGTGT GTCACACCTA TACTACAGTC CTAAGTCGAC TTCTCGTTCA  
-----  
+1 -----  
701 GGGATGAGTC CATCTTCACG AAAGGCTGCA TCCAGGCGCT GGAAAGCTGG  
    CCCTACTCAG GTAGAAGTGC TTTCCGACGT AGGTCCGCGA CCTTTCGACC  
-----  
+1 -----  
751 CTCCCGCGGA ACATTTACAT TGTGGCTGGC GTCTTCATCG CCATCTCGCT  
    GAGGGCGCCT TGTAATGTA ACACCGACCG CAGAAGTAGC GGTAGAGCGA  
-1 <-----  
-----  
+1 -----  
801 GTTGCAGATA TTTGGCATCT TCCTGGCAAG GACGCTGATC TCAGACATCG  
    CAACGTCTAT AAACCGTAGA AGGACCGTTC CTGCGACTAG AGTCTGTAGC  
-1 -----  
-----  
+1 ----->  
851 AGGCAGTGAA GGCCGGCCAT CACTTCTGAG GAGCAGAGTT GAGGGAGCCG  
    TCCGTCACTT CCGGCCCGTA GTGAAGACTC CTCGTCTCAA CTCCCTCGGC  
-1 -----  
-----  
901 AGCTGAGCCA CGCTGGGAGG CCAGAGCCTT TCTTGCCAT CAGCCCTACG  
    TCGACTCGGT GCGACCCTCC GGTCTCGGAA AGAGACGGTA GTCGGGATGC  
-1 -----  
-----  
+1 -----  
951 TCCAGAGGGA GAGGAGCCGA CACCCCAGA GCCAGTGCCC CATCTTAAGC  
    AGGTCTCCCT CTCCTCGGCT GTGGGGGTCT CGGTCACGGG GTAGAATTCG  
-1 -----  
-----  
+1 -----  
1001 ATCAGCGTGA CGTGACCTCT CTGTTTCTGC TTGCTGGTGC TGAAGACCAA  
    TAGTCGCACT GCACTGGAGA GACAAAGACG AACGACCACG ACTTCTGGTT  
-----  
+1 -----  
1051 GGGTCCCCCT TGTTACCTGC CAAAATTGT GACTGCATCC CTCTGGAGTC  
    CCCAGGGGGA ACAATGGACG GGTGGAACA CTGACGTAGG GAGACCTCAG  
-----  
+1 -----  
1101 TACCCAGAGA CAGAGAATGT GTCTTTATGT GGGAGTNGTG ACTCTGAAAG  
    ATGGGTCTCT GTCTCTTACA CAGAAATACA CCCTCANCAC TGAGACTTTC  
-1 <-----  
-----  
+1 -----  
PstI  
~~~~~  
1151 ACAGAGAGGG CTCCTGTGGS TGCCAGGAGG GCTTGACTCA GACCCCTGCG  
    TGTCTCTCCC GAGGACACCS ACGGTCCTCC CGAACTGAGT CTGGGGGACG  
-1 -----
```

FIGURE 2C

```
+1 -----  
PstI  
~~  
1201 AGCTCAAGCA TGTYTGCAGG ACACCCTGGT CCCYTYTCCA YTGGCWTCCA  
TCGAGTTCGT ACARACGTCC TGTGGGACCA GGGRARAGGT RACCGWAGGT  
-1 -----  
  
+1 ----->  
1251 GACATCTGCT TTGGGTCATC CACATCTGTG GGTINGGCCGT GGGTAGAGGG  
CTGTAGACGA AACCCAGTAG GTGTAGACAC CCANCCGGCA CCCATCTCCC  
-1 -----  
  
1301 ACCCACAGGC GTGGACAGGG CATCTCTCTC CATCAAGCAA AGCAGCATGG  
TGGGTGTCCG CACCTGTCCC GTAGAGAGAG GTAGTTCGTT TCGTCGTACC  
-1 -----[  
  
1351 GGGGCCTTGC CGTAAACGGG AGGCGNGACG TTGGCCC  
CCCCGGAACG GCATTGCCC TCCGCNCTGC AACCGGG
```

FIGURE 3

```
1  MHYYRYSNAK VSCWYKYLLE SYNIIFWLAG VVFLGVGLWA WSEKGVLSDL
51  TKVTRMHGID PVVLVLMVGV VMFTLGFAAGC VGALRENICL LNFFCGTIVL
101 IFFLELAVAV LAFLFQDWVR DRFREFFESN IKSyrDDIDL QNLIDSLQKA
151 NQCCGAYGPE DWDLNVYFNC SGASYSREKC GVPFSCCVPD PAQKVNTQC
201 GYDVRIQLKS KWDESIFTKG CIQALESWLP RNIYIVAGVF IAISLLQIFG
251 IFLARTLISD IEAVKAGHHF
```

FIGURE 4

NTSP5:P104	CHIR22-1	TGCAGCCTTTTCGTGAAGATGGACTC	25 (7-11-7)
NTSP5:P727	CHIR22-2	CCCCATGCTGCTTTGCTTGATGGAG	25 (7-11-7)
NTSP5:P285	CHIR22-3	GCTCAGCTCGGCTCCCTCAACTC	23 (7-9-7)
NTSP5:P456	CHIR22-4	CACAAGTTTGGGCAGGTAACAAGGG	25 (7-11-7)
NTSP5:P395	CHIR22-5	AGAGGTCACGTCACGCTGATGCTTA	25 (7-11-7)
NTSP5:P104	CHIR22-1RC	CTCAGGTAGAAGTGCTTTCCGACGT	25 (7-11-7)
NTSP5:P727	CHIR22-2RC	GAGGTAGTTCGTTTCGTCGTACCCC	25 (7-11-7)
NTSP5:P285	CHIR22-3RC	CTCAACTCCCTCGGCTCGACTCG	23 (7-9-7)
NTSP5:P456	CHIR22-4RC	GGGAACAATGGACGGGTTTGAACAC	25 (7-11-7)
NTSP5:P395	CHIR22-5RC	ATTCGTAGTCGCACTACGCTGGAGA	25 (7-11-7)

FIGURE 5

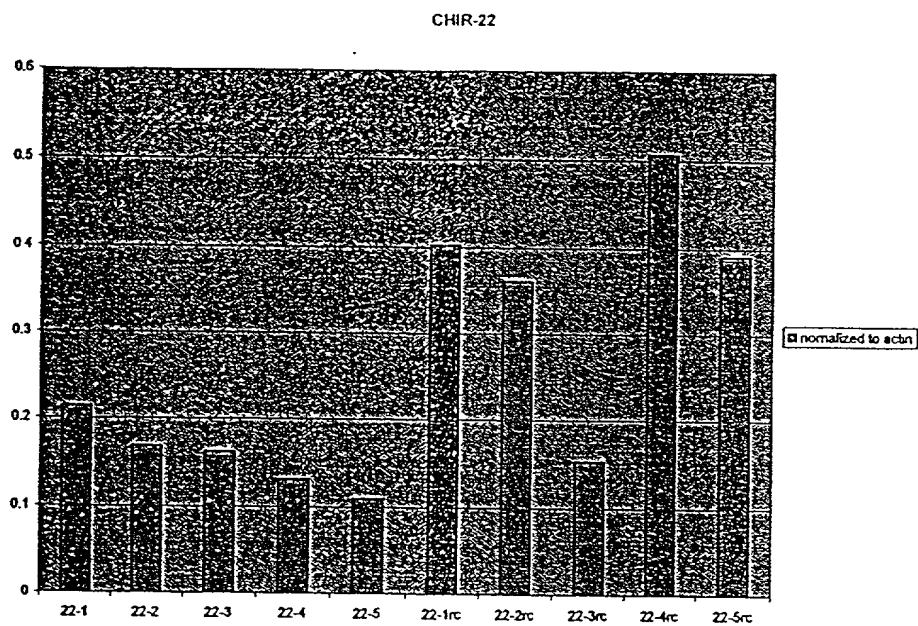


FIGURE 6

